



SEQUENCE LISTING

<110> Martin, John Francis
Yla-Herttuala, Seppo
Barker, Stephen George Edward

<120> Therapeutic Use of an Agent That Stimulates NO or Prostacyclin Production and Delivery Device

<130> GJE-30

<140> US 09/297,486

<141> 1999-04-30

<150> PCT/GB97/03015

<151> 1997-11-03

<150> GB 9622852.3

<151> 1996-11-01

<150> GB 9709494.0

<151> 1997-05-09

<150> GB 9717791.9

<151> 1997-08-21

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tac ctc cac cat gcc aag tgg tcc cag gct gca ccc atg gca gaa gga	96
Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly	
20 25 30	
gga ggg cag aat cat cac gaa gtg gtg aag ttc atg gat gtc tat cag	144
Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln	
35 40 45	
cgc agc tac tgc cat cca atc gag acc ctg gtg gac atc ttc cag gag	192
Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu	
50 55 60	

tac cct gat gag atc gag tac atc ttc aag cca tcc tgt gtg ccg ctg 240
 Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg gag tgt gtg ccc 288
 Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

act gag gag tcc aac atc acc atg cag att atg cgg atc aaa cct cac 336
 Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

caa ggc cag cac ata gga gag atg agc ttc cta cag cac aac aaa tgt 384
 Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

gaa tgc aga cca aag aaa gat aga gca aga caa gaa aaa tgt gac aag 432
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Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
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Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
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Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Cys Asp Lys
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tac ctc cac cat gcc aag tgg tcc cag gct gca ccc atg gca gaa gga	96
Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly	
20 25 30	
gga ggg cag aat cat cac gaa gtg gtg aag ttc atg gat gtc tat cag	144
Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln	
35 40 45	
cgc agc tac tgc cat cca atc gag acc ctg gtg gac atc ttc cag gag	192
Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu	
50 55 60	
tac cct gat gag atc gag tac atc ttc aag cca tcc tgt gtg ccg ctg	240
Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu	
65 70 75 80	
atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg gag tgt gtg ccc	288
Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro	
85 90 95	
act gag gag tcc aac atc acc atg cag att atg cgg atc aaa cct cac	336
Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His	
100 105 110	
caa ggc cag cac ata gga gag atg agc ttc cta cag cac aac aaa tgt	384
Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys	
115 120 125	
gaa tgc aga cca aag aaa gat aga gca aga caa gaa aaa ccc tgt ggg	432
Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Pro Cys Gly	
130 135 140	

cct tgc tca gag cgg aga aag cat ttg ttt gta caa gat ccg cag acg 480
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 145 150 155 160

tgt aaa tgt tcc tgc aaa aac aca gac tcg cgt tgc aag gcg agg cag 528
 Cys Lys Cys Ser Cys Lys Asn Thr Asp Ser Arg Cys Lys Ala Arg Gln
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Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
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Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Pro Cys Gly
 130 135 140

Pro Cys Ser Glu Arg Arg Lys His Leu Phe Val Gln Asp Pro Gln Thr
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tac ctc cac cat gcc aag tgg tcc cag gct gca ccc atg gca gaa gga	96
Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly	
20 25 30	
gga ggg cag aat cat cac gaa gtg gtg aag ttc atg gat gtc tat cag	144
Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln	
35 40 45	
cgc agc tac tgc cat cca atc gag acc ctg gtg gac atc ttc cag gag	192
Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu	
50 55 60	
tac cct gat gag atc gag tac atc ttc aag cca tcc tgt gtg ccg ctg	240
Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu	
65 70 75 80	
atg cga tgc ggg ggc tgc tgc aat gac gag ggc ctg gag tgt gtg ccc	288
Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro	
85 90 95	
act gag gag tcc aac atc acc atg cag att atg cgg atc aaa cct cac	336
Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His	
100 105 110	
caa ggc cag cac ata gga gag atg agc ttc cta cag cac aac aaa tgt	384
Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys	
115 120 125	
gaa tgc aga cca aag aaa gat aga gca aga caa gaa aaa aaa tca gtt	432
Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val	
130 135 140	
cga gga aag gga aag ggg caa aaa cga aag cgc aag aaa tcc cgg tat	480
Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr	
145 150 155 160	
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Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His	
165 170 175	

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gac tcg cgt tgc aag gcg agg cag ctt gag tta aac gaa cgt act tgc 624
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Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly
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Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
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Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
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Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
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Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
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Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val
 130 135 140

Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr
 145 150 155 160

Lys Ser Trp Ser Val Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys His
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Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn Thr
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Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr Cys
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Arg Cys Asp Lys Pro Arg Arg
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Tyr Leu His His Ala Lys Trp Ser Gln Ala Ala Pro Met Ala Glu Gly	
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gga ggg cag aat cat cac gaa gtg gtg aag ttc atg gat gtc tat cag	144
Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln	
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Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu	
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Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu	
65 70 75 80	
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Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro	
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act gag gag tcc aac atc acc atg cag att atg cgg atc aaa cct cac	336
Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His	
100 105 110	
caa ggc cag cac ata gga gag atg agc ttc cta cag cac aac aaa tgt	384
Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys	
115 120 125	
gaa tgc aga cca aag aaa gat aga gca aga caa gaa aaa aaa tca gtt	432
Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val	
130 135 140	

cga gga aag gga aag ggg caa aaa cga aag cgc aag aaa tcc cgg tat 480
 Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr
 145 150 155 160

aag tcc tgg agc gtg tac gtt ggt gcc cgc tgc tgt cta atg ccc tgg 528
 Lys Ser Trp Ser Val Tyr Val Gly Ala Arg Cys Cys Leu Met Pro Trp
 165 170 175

agc ctc cct ggc ccc cat ccc tgt ggg cct tgc tca gag cgg aga aag 576
 Ser Leu Pro Gly Pro His Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys
 180 185 190

cat ttg ttt gta caa gat ccg cag acg tgt aaa tgt tcc tgc aaa aac 624
 His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn
 195 200 205

aca gac tcg cgt tgc aag gcg agg cag ctt gag tta aac gaa cgt act 672
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 210 215 220

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Gly Gly Gln Asn His His Glu Val Val Lys Phe Met Asp Val Tyr Gln
 35 40 45

Arg Ser Tyr Cys His Pro Ile Glu Thr Leu Val Asp Ile Phe Gln Glu
 50 55 60

Tyr Pro Asp Glu Ile Glu Tyr Ile Phe Lys Pro Ser Cys Val Pro Leu
 65 70 75 80

Met Arg Cys Gly Gly Cys Cys Asn Asp Glu Gly Leu Glu Cys Val Pro
 85 90 95

Thr Glu Glu Ser Asn Ile Thr Met Gln Ile Met Arg Ile Lys Pro His
 100 105 110

Gln Gly Gln His Ile Gly Glu Met Ser Phe Leu Gln His Asn Lys Cys
 115 120 125

Glu Cys Arg Pro Lys Lys Asp Arg Ala Arg Gln Glu Lys Lys Ser Val
 130 135 140

Arg Gly Lys Gly Lys Gly Gln Lys Arg Lys Arg Lys Lys Ser Arg Tyr
 145 150 155 160

Lys Ser Trp Ser Val Tyr Val Gly Ala Arg Cys Cys Leu Met Pro Trp
 165 170 175

Ser Leu Pro Gly Pro His Pro Cys Gly Pro Cys Ser Glu Arg Arg Lys
 180 185 190

His Leu Phe Val Gln Asp Pro Gln Thr Cys Lys Cys Ser Cys Lys Asn
 195 200 205

Thr Asp Ser Arg Cys Lys Ala Arg Gln Leu Glu Leu Asn Glu Arg Thr
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Cys Arg Cys Asp Lys Pro Arg Arg
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<210> 10
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